



Sequence Listing US10069427.txt

SEQUENCE LISTING

<110> Famodu, Omolayo O.
Kinney, Anthony J.

<120> Genes Encoding Sterol Delta-14 Reductase in Plants

<130> 2119-4293

<140> 10/069,427

<141>

<150> 60/156,820

<151> 1999-09-30

<160> 10

<170> Microsoft Office 95

<210> 1

<211> 427

<212> DNA

<213> Glycine max

<220>

<221> unsure

<222> (360)

<223> n=a,c,g or t

<400> 1

```
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aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg atccattctc 120
cctggaaaac ttgttccttg cgttgcacta ctcgatggaa ctcgcttaca ctattgctgc 180
aatggtctgc tctcgcttct tctgttgggt gcacttctcg ggatcggtgc caagatgggt 240
tttgtgtctc ccactgccat atcaaacaga ggacttgagc tgctgtccac aacttttgcc 300
ttcagttttc ttgtaaccct gatattgcat tttccgggt gcaagtcaca aagtaaagg 360
tcatactaa agcctcatct cagtgggaac ctgatacacg attggtgggt tgggaataca 420
actaaaa
```

<210> 2

<211> 126

<212> PRT

<213> Glycine max

<400> 2

```
Leu Gln Ala Leu Thr Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly
 1          5          10          15
```

```
Phe Phe Thr Tyr Leu Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu
      20          25          30
```

```
Val Pro Gly Val Ala Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys
      35          40          45
```

```
Asn Gly Leu Leu Ser Leu Leu Leu Val Ala Leu Leu Gly Ile Gly
      50          55          60
```

```
Ala Lys Met Gly Phe Val Ser Pro Thr Ala Ile Ser Asn Arg Gly Leu
      65          70          75          80
```

```
Glu Leu Leu Ser Thr Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile
```

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85

90

95

Leu His Phe Ser Gly Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys
 100 105 110

Pro His Leu Ser Gly Asn Leu Ile His Asp Trp Trp Phe Gly
 115 120 125

<210> 3

<211> 667

<212> DNA

<213> Zea mays

<400> 3

```
ccacgcgtcc ggaagaacaa agtagagctg tcccttttgt ctggtctagc taacttatgc 60
atctttctta ttggctacct agtggtccga ggagctaaca agcaaaaaca tgtgttcaag 120
aaggaccca aagctcctat atggggaaaa cctcccaaag ttgtcggggg aaagctacta 180
gcatctgggt actggggcat cgcaaggcac tgcaattatc tcggagacct gctgctagca 240
ctttcgttca gcttgccctg tggagtgagt tccgtggtcc catacttcta cccacgtac 300
ctgctcattc tactggctct gagggaaaag cgcgatgagg cgagggtgctc gcagaagtac 360
agggagatct gggcagagta ctgcaagctc gtgccgtgga ggatcctgcc ttatgtgtac 420
tgaagagacg gtagaaacca aggcagctca tggccctggg ccagctgtaa acctatttt 480
gtttgccctt aaccagttgg tgaatgttga tgtagcactc ggtaaactgt gaccgtgcaa 540
acttttgtaa ttgttgggtc atacatgttt ggaatcgtga atcagaccgc ctacttgggt 600
ggcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 660
aaaaaag
```

<210> 4

<211> 140

<212> PRT

<213> Zea mays

<400> 4

Pro Arg Val Arg Lys Asn Lys Val Glu Leu Ser Leu Leu Ser Gly Leu
 1 5 10 15

Ala Asn Leu Cys Ile Phe Leu Ile Gly Tyr Leu Val Phe Arg Gly Ala
 20 25 30

Asn Lys Gln Lys His Val Phe Lys Lys Asp Pro Lys Ala Pro Ile Trp
 35 40 45

Gly Lys Pro Pro Lys Val Val Gly Gly Lys Leu Leu Ala Ser Gly Tyr
 50 55 60

Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Leu Leu Ala
 65 70 75 80

Leu Ser Phe Ser Leu Pro Cys Gly Val Ser Ser Val Val Pro Tyr Phe
 85 90 95

Tyr Pro Thr Tyr Leu Leu Ile Leu Leu Val Leu Arg Glu Arg Arg Asp
 100 105 110

Glu Ala Arg Cys Ser Gln Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Cys
 115 120 125

Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
 130 135 140

<210> 5

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<211> 1631
<212> DNA
<213> Glycine max

<400> 5
ccgcgttgga atttgcccat ctaaaacctc aatcttttac tgaaaagtct caactttgaa 60
ctcactcgaa gtgatgatgg agtcacacgt ggatctagggt tttctccttc aagctctcac 120
tccatcttgg aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg 180
atccattctc cctggaaaac ttgttcctgg cgttgcacta ctcgatggaa ctcgtctaca 240
ctattgctgc aatgggtctgc tctcgcttct tctgttgggt gcacttctcg ggatcgggtgc 300
caagatgggt tttgtgtctc ccactgccat atcagacaga ggacttgagc tgctgtccac 360
aacttttgcc ttcagttttc ttgtaaccct gatattgcat tttccgggt gcaagtcaca 420
aagtaaagggt tcatcactaa agcctcatct cagtggaaac ctgatacacg attgggtggt 480
tggatataca ctaaattccac agttcatggg tatcgacctc aaatttttct ttgtagagc 540
tggaatgatg ggaatggctac ttatcaattt atctattctt atgaagagca ttcaagatgg 600
tactttgagc cagtcaatga ttctctacca gctattctgt gcactataca tcctggacta 660
ttttgtacat gaagagtaca tgacatccac ctgggacata attgcagaga gactgggctt 720
catgttggtc tttggagatt tagtgtggat tcttttctct ttcagcatac agggatgggtg 780
gctcttgatg aacagtgtgg agttaacacc agctgccatt gtagctaatt gctttgtgtt 840
cctgattgga tacatgggat ttcgaggagc aaacaagcaa aagcatgtgt tcaaaaagaa 900
tccaaaggct cctatctggg gtaagcctcc aaaagtcatt ggtggaaagc tacttgcttc 960
tggattattg ggtattgcta gacactgtaa ttacctaggg gatttgatgc ttgctctctc 1020
ctttagctta ccatgtggga taagtccacc aattccatac ttctatccaa tttatcttct 1080
tattctgtta atctggagag agagaaggga tgaagctcgt tgcgccgaga agtatagaga 1140
gatatgggccc gagtatcgta aacttggtcc atggagaata ttgccttacg tttattagga 1200
tgaaaaaaaa aagggtcttc ccatgaattc ttcattctgc cgatgttatt aagcacttcg 1260
atgtaaattg gttcttgctc ttgtggtttc aatcttggat cttttcttat tgagccatgt 1320
agctgcagga gagtgtttcg agggatttat cttaccatct atatttgtgt atcattatgc 1380
tgcagcctgc aggccttcat tttcaatgg ccaactcttt ttgacttggt ctatttgttt 1440
ttagatgaga atttcatggt caaagctcct aggcctaaaa aaacagtgtc atgttctatg 1500
ggaagtgcag gaagcaattc ggggactgca ggaagcaatt gcctttacat tgatatgctc 1560
aatggtactt taggcccttt aatgttcttg cttttcattt gtgagttatt attggcccca 1620
tttcatttgc a 1631

<210> 6
<211> 374
<212> PRT
<213> Glycine max

<400> 6
Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
1 5 10 15
Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
20 25 30
Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
35 40 45
Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
50 55 60
Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
65 70 75 80
Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
85 90 95
Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
100 105 110
Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly

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```

115      120      125
Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
130      135      140
Met Gly Ile Asp Leu Lys Phe Phe Phe Val Arg Ala Gly Met Met Gly
145      150      155      160
Trp Leu Leu Ile Asn Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly
165      170      175
Thr Leu Ser Gln Ser Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr
180      185      190
Ile Leu Asp Tyr Phe Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp
195      200      205
Ile Ile Ala Glu Arg Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val
210      215      220
Trp Ile Pro Phe Ser Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn
225      230      235      240
Ser Val Glu Leu Thr Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe
245      250      255
Leu Ile Gly Tyr Met Val Phe Arg Gly Ala Asn Lys Gln Lys His Val
260      265      270
Phe Lys Lys Asn Pro Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val
275      280      285
Ile Gly Gly Lys Leu Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His
290      295      300
Cys Asn Tyr Leu Gly Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro
305      310      315      320
Cys Gly Ile Ser Ser Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu
325      330      335
Ile Leu Leu Ile Trp Arg Glu Arg Arg Asp Glu Ala Arg Cys Ala Glu
340      345      350
Lys Tyr Arg Glu Ile Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg
355      360      365
Ile Leu Pro Tyr Val Tyr
370

```

<210> 7
 <211> 1364
 <212> DNA
 <213> Glycine max

<400> 7
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 gtgatgatgg agtcacacgt ggatctaggt tttctccttc aagctctcac tccatcttgg 120
 aactccgttc ctttgcttgt ggggttcttc acttacttgg ccgttgctgg atccattctc 180
 cctggaaaac ttgttcttgg cgttgcacta ctcgatggaa ctcgtctaca ctattgctgc 240

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```

aatggtctgc tctcgcttct tctgttggtt gcacttctcg ggatcgggtg caagatgggt 300
tttgtgtctc ccactgccat atcagacaga ggacttgagc tgctgtccac aacttttgcc 360
ttcagttttc ttgtaaccct gatattgcat ttttccggtt gcaagtcaca aagtaaagg 420
tcatcactaa agcctcatct cagtggaaac ctgatacacg attggtgggt tggatatacaa 480
ctaaatccac agttcatggg tatcgacctc aaagctggaa tgatgggatg gctacttatc 540
aatttatcta ttcttatgaa gagcattcaa gatggtactt tgagccagtc aatgattctc 600
taccagctat tctgtgcaat atacatcctg gactattttg tacatgaaga gtacatgaca 660
tccacctggg acataattgc agagagactg ggcttcatgt tggcttttgg agatttagtg 720
tggattcctt tctctttcag catacagggg tgggtggctct tgatgaacag tgtggagtta 780
acaccagctg ccattgtagc taattgcttt gtgttcctga ttggatacat ggtatttcga 840
ggagcaaaca agcaaaaagca tgtgttcaaa aagaatccaa aggtctctat ctggggtaag 900
cctccaaaag tcattggtgg aaagctactt gcttctgggt attgggggtat tgctagacac 960
tgtaattacc taggggattt gatgcttgct ctctccttta gcttaccatg tgggataagt 1020
tcaccaattc catacttcta tccaatttat cttcttattc tgtaaatctg gagagagaga 1080
acggatgaag ctggttgccg cgagaagtat agagagatat gggccgagta tcgtaaactt 1140
gttccatgga gaattattgc ttacgtttat taggatgaaa aaaaaaaggg cttcaccatg 1200
aattcttcat cttgccgatg ttattaagca cttcgatgta aattggttct tgttcttctg 1260
gtttcaatct tggatctttt cttattgagc catgtagctg caggagagtg tttcgaggga 1320
tttatcttac catctatatt tgtgtaaaaa aaaaaaaaaa aaaa 1364

```

<210> 8
 <211> 369
 <212> PRT
 <213> Glycine max

<400> 8
 Met Met Glu Ser His Val Asp Leu Gly Phe Leu Leu Gln Ala Leu Thr
 1 5 10 15
 Pro Ser Trp Asn Ser Val Pro Leu Leu Val Gly Phe Phe Thr Tyr Leu
 20 25 30
 Ala Val Ala Gly Ser Ile Leu Pro Gly Lys Leu Val Pro Gly Val Ala
 35 40 45
 Leu Leu Asp Gly Thr Arg Leu His Tyr Cys Cys Asn Gly Leu Leu Ser
 50 55 60
 Leu Leu Leu Leu Val Ala Leu Leu Gly Ile Gly Ala Lys Met Gly Phe
 65 70 75 80
 Val Ser Pro Thr Ala Ile Ser Asp Arg Gly Leu Glu Leu Leu Ser Thr
 85 90 95
 Thr Phe Ala Phe Ser Phe Leu Val Thr Leu Ile Leu His Phe Ser Gly
 100 105 110
 Cys Lys Ser Gln Ser Lys Gly Ser Ser Leu Lys Pro His Leu Ser Gly
 115 120 125
 Asn Leu Ile His Asp Trp Trp Phe Gly Ile Gln Leu Asn Pro Gln Phe
 130 135 140
 Met Gly Ile Asp Leu Lys Ala Gly Met Met Gly Trp Leu Leu Ile Asn
 145 150 155 160
 Leu Ser Ile Leu Met Lys Ser Ile Gln Asp Gly Thr Leu Ser Gln Ser
 165 170 175
 Met Ile Leu Tyr Gln Leu Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe
 180 185 190

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Val His Glu Glu Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg
195 200 205
Leu Gly Phe Met Leu Val Phe Gly Asp Leu Val Trp Ile Pro Phe Ser
210 215 220
Phe Ser Ile Gln Gly Trp Trp Leu Leu Met Asn Ser Val Glu Leu Thr
225 230 235 240
Pro Ala Ala Ile Val Ala Asn Cys Phe Val Phe Leu Ile Gly Tyr Met
245 250 255
Val Phe Arg Gly Ala Asn Lys Gln Lys His Val Phe Lys Lys Asn Pro
260 265 270
Lys Ala Pro Ile Trp Gly Lys Pro Pro Lys Val Ile Gly Gly Lys Leu
275 280 285
Leu Ala Ser Gly Tyr Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly
290 295 300
Asp Leu Met Leu Ala Leu Ser Phe Ser Leu Pro Cys Gly Ile Ser Ser
305 310 315 320
Pro Ile Pro Tyr Phe Tyr Pro Ile Tyr Leu Leu Ile Leu Leu Ile Trp
325 330 335
Arg Glu Arg Thr Asp Glu Ala Arg Cys Ala Glu Lys Tyr Arg Glu Ile
340 345 350
Trp Ala Glu Tyr Arg Lys Leu Val Pro Trp Arg Ile Leu Pro Tyr Val
355 360 365

Tyr
369

<210> 9
<211> 430
<212> PRT
<213> Ascobolus immersus

<400> 9
Met Gly Gly Lys Asp Tyr Glu Phe Gly Gly Pro Ile Gly Thr Gly Val
1 5 10 15
Leu Met Leu Ile Leu Pro Pro Ile Ser His Tyr Leu His Phe Leu Ile
20 25 30
Thr Pro Arg Gly Ala Pro Pro Pro Glu Phe Trp Ser Ala Pro Leu Glu
35 40 45
Thr Leu Lys Ser Val Thr Pro Thr Phe Ser Ser Leu Phe Ser Leu His
50 55 60
Ala Thr Leu Ala Val Ala Ala Tyr Tyr Leu Leu Val Ala Leu Met
65 70 75 80
Tyr Val Leu Pro Ala Glu Ile Ala Glu Gly Val Val Leu Lys Asp Gly
85 90 95
Ser Arg Leu Lys Tyr Arg Cys Asn Ala Phe Thr Thr Phe Leu Val Phe
100 105 110

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Phe Thr Phe Leu Gly Thr Met Thr Val Leu Glu Gly Pro Thr Trp Trp
 115 120 125
 Phe Trp Ser Tyr Leu Thr Asp Asn Phe Ala Gln Leu Gln Ser Ala Ser
 130 135 140
 Ile Val Phe Ser Tyr Ala Met Ser Leu Trp Val Tyr Ile Arg Ser Tyr
 145 150 155 160
 Arg Pro Met Pro Lys Gly Lys Glu Val Ile Leu Ser Pro Val Gly Phe
 165 170 175
 Lys Gly Asn His Ile His Asp Phe Trp Met Gly Arg Glu Leu Asn Pro
 180 185 190
 Arg Ile Gly Glu Trp Leu Asp Ile Lys Gln Leu His Glu Leu Arg Pro
 195 200 205
 Gly Leu Met Gly Trp Ile Leu Phe Asn Leu Ala Trp Thr Val Lys Gln
 210 215 220
 Tyr Asn Thr His Gly Phe Val Ser Asp Ser Ile Val Leu Val Asn Leu
 225 230 235 240
 Phe Glu Thr Trp Tyr Val Val Asp Ala Leu Trp Asn Glu Ser Lys Val
 245 250 255
 Leu Thr Thr Met Asp Ile Thr Thr Asp Gly Leu Gly Val Met Leu Leu
 260 265 270
 Phe Gly Asn Ala Val Trp Val Pro Phe Met Tyr Cys Leu Gln Ala Arg
 275 280 285
 Tyr Leu Ala Ser Phe Pro Val His Leu Gly Leu Leu Gly Ile Ala Gly
 290 295 300
 Val Leu Ala Val Gln Phe Thr Gly Tyr Ala Ile Phe Arg Gly Ala Asn
 305 310 315 320
 Asn Gln Lys Asn Ala Phe Arg Thr Asn Pro Ala Asp Pro Ala Val Ser
 325 330 335
 His Leu Lys Phe Met Thr Thr Lys Ser Gly Ser Lys Leu Leu Ile Ser
 340 345 350
 Gly Trp Trp Gly Val Ala Arg His Val Asn Tyr Phe Gly Asp Trp Ile
 355 360 365
 Met Ala Trp Ser Tyr Cys Leu Thr Thr Gly Phe Asn Thr Pro Leu Thr
 370 375 380
 Tyr Phe Tyr Val Ile Tyr Phe Gly Ile Leu Leu Leu His Arg Asp Arg
 385 390 395 400
 Arg Asp Glu Ala Lys Cys Arg Glu Lys Tyr Gly Lys Asp Trp Asp Arg
 405 410 415
 Tyr Cys Lys Val Val Lys Trp Arg Ile Ile Pro Gly Ile Tyr
 420 425 430

<210> 10
 <211> 365

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<212> PRT

<213> Arabidopsis thaliana

<400> 10

```

Met Asp Leu Gly Val Leu Leu Pro Ser Leu Gln Ser Val Tyr Val Leu
 1          5          10          15
val Phe Tyr Phe Val Tyr Leu Ala Val Ala Gly Glu Ile Leu Pro Gly
          20          25          30
Lys Val Ile Arg Gly Val Leu Leu Ser Asp Gly Ser Gln Leu Arg Tyr
          35          40          45
Arg Cys Asn Gly Leu Leu Ala Leu Ile Leu Leu Val Ala Ile Leu Gly
          50          55          60
Ile Cys Ala Lys Leu Gly Ile Val Ser Pro Leu Val Val Ala Asp Arg
          65          70          75          80
Gly Leu Glu Leu Leu Ser Ala Thr Phe Ile Phe Cys Val Leu Val Thr
          85          90          95
Leu Ala Leu Tyr Val Thr Gly Arg Ser Ser Ser Asn Lys Gly Ser Ser
          100          105          110
Leu Lys Pro His Val Ser Gly Asn Leu Val His Asp Trp Trp Phe Gly
          115          120          125
Ile Gln Leu Asn Pro Gln Phe Met Ser Ile Asp Leu Lys Phe Phe Phe
          130          135          140
Val Arg Ala Gly Met Met Gly Trp Leu Leu Ile Asn Leu Ser Ile Leu
          145          150          155          160
Ala Lys Ser Val Gln Asp Gly Ser Leu Ser Gln Ser Met Ile Leu Tyr
          165          170          175
Gln Ile Phe Cys Ala Leu Tyr Ile Leu Asp Tyr Phe Val His Glu Glu
          180          185          190
Tyr Met Thr Ser Thr Trp Asp Ile Ile Ala Glu Arg Leu Gly Phe Met
          195          200          205
Leu Val Phe Gly Asp Leu Leu Trp Ile Pro Phe Thr Phe Ser Ile Gln
          210          215          220
Gly Trp Trp Leu Leu His Asn Lys Val Glu Leu Thr Val Pro Ala Ile
          225          230          235          240
Val Val Asn Cys Leu Val Phe Leu Ile Gly Tyr Met Val Phe Arg Gly
          245          250          255
Ala Asn Lys Gln Lys His Ile Phe Lys Lys Asn Pro Lys Thr Pro Ile
          260          265          270
Trp Gly Lys Pro Pro Val Val Val Gly Gly Lys Leu Leu Val Ser Gly
          275          280          285
Tyr Trp Gly Ile Ala Arg His Cys Asn Tyr Leu Gly Asp Leu Met Leu
          290          295          300
Ala Leu Ser Phe Ser Leu Pro Cys Gly Ile Ser Ser Pro Val Pro Tyr
          305          310          315          320

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Phe Tyr Pro Ile Tyr Leu Leu Ile Leu Leu Ile Trp Arg Glu Arg Arg
325 330 335
Asp Glu Val Arg Cys Ala Glu Lys Tyr Lys Glu Ile Trp Ala Glu Tyr
340 345 350
Leu Arg Leu Val Pro Trp Arg Ile Leu Pro Tyr Val Tyr
355 360 365